

10/590705

SEQUENCE LISTING

<110> KYOWA HAKKO KOGYO CO., LTD

<120> Method for producing amino acid

<130> 1657

<160> 16

<170> PatentIn Ver. 3.1

<210> 1

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA

<400> 1

ctgcttgccc tgcaggtgca ccagcaaacg

30

<210> 2

<211> 30

<212> DNA

<213> Artificial

<220>

<223> Synthetic DNA

<400> 2

cgagctgctg gacaaccagg aattcagcgg

30

<210> 3

<211> 1404

<212> DNA

<213> Corynebacterium glutamicum ATCC13032

<220>

<221> CDS

<222>

<400> 3

atg	tca	ggt	aac	cca	acc	cgc	ccc	gaa	ggc	ggc	cgt	cac	cac	gtc	gtc	48
Met	Ser	Val	Asn	Pro	Thr	Arg	Pro	Glu	Gly	Gly	Arg	His	His	Val	Val	
1				5					10					15		

gtc	atc	ggt	tct	ggt	ttt	ggt	ggc	ctt	ttt	gct	gcc	aag	aac	ctg	gcc	96
Val	Ile	Gly	Ser	Gly	Phe	Gly	Gly	Leu	Phe	Ala	Ala	Lys	Asn	Leu	Ala	
			20					25					30			

aag Lys	gca Ala	gac Asp 35	gtc Val	gat Asp	gtc Val	act Thr	ctg Leu 40	att Ile	gac Asp	cgc Arg	acc Thr	aac Asn 45	cac His	cac His	ctc Leu	144
ttc Phe	cag Gln 50	cca Pro	ctg Leu	ctg Leu	tac Tyr	caa Gln 55	gtg Val	gca Ala	acc Thr	ggt Gly	atc Ile 60	ctc Leu	tcc Ser	tcc Ser	ggt Gly	192
gaa Glu 65	atc Ile	gca Ala	cct Pro	tcc Ser	act Thr 70	cga Arg	cag Gln	atc Ile	ctg Leu	ggc Gly 75	tcc Ser	cag Gln	gaa Glu	aac Asn	gtc Val 80	240
aac Asn	gtc Val	atc Ile	aag Lys	ggc Gly 85	gaa Glu	gtc Val	acc Thr	gac Asp	atc Ile 90	aac Asn	gtc Val	gag Glu	tcc Ser	cag Gln 95	act Thr	288
gtg Val	acc Thr	gcc Ala	tcc Ser 100	ctg Leu	ggc Gly	gag Glu	ttc Phe	acc Thr 105	cgc Arg	gtt Val	ttt Phe	gag Glu	tac Tyr 110	gat Asp	tcc Ser	336
ttg Leu	gtc Val	gtt Val 115	ggt Gly	gct Ala	ggc Gly	gca Ala	ggt Gly 120	cag Gln	tcc Ser	tac Tyr	ttc Phe	ggc Gly 125	aat Asn	gat Asp	cac His	384
ttc Phe 130	gct Ala	gag Glu	ttc Phe	gca Ala	cct Pro	ggc Gly 135	atg Met	aag Lys	tcc Ser	atc Ile	gac Asp 140	gat Asp	gca Ala	ctg Leu	gag Glu	432
att Ile 145	cgt Arg	gca Ala	cgc Arg	atc Ile	atc Ile 150	ggt Gly	gct Ala	ttc Phe	gag Glu	cgc Arg 155	gct Ala	gag Glu	atc Ile	tgc Cys	gag Glu 160	480
gat Asp	cca Pro	gct Ala	gag Glu	cgc Arg 165	gaa Glu	cgc Arg	ctg Leu	ctc Leu	acc Thr 170	ttc Phe	gtc Val	gtt Val	gtt Val	ggc Gly 175	gct Ala	528
ggc Gly	cca Pro	acc Thr	ggt Gly 180	gtt Val	gag Glu	ctt Leu	gct Ala	ggc Gly 185	cag Gln	ttg Leu	gct Ala	gag Glu	atg Met 190	gct Ala	cac His	576
cgc Arg	acc Thr	ctt Leu 195	gct Ala	ggt Gly	gag Glu	tac Tyr	aag Lys 200	aac Asn	ttc Phe	aac Asn	acc Thr	aac Asn 205	tcc Ser	gca Ala	aag Lys	624
atc Ile 210	atc Ile	ctg Leu	ctt Leu	gat Asp	ggt Gly	gct Ala 215	cca Pro	cag Gln	gtt Val	ctt Leu	cct Pro 220	cca Pro	ttc Phe	ggt Gly	aag Lys	672
cgc	cta	ggc	cgc	aac	gca	cag	cgc	acc	ctg	gaa	aag	atg	ggt	gtc	aac	720

Arg 225	Leu	Gly	Arg	Asn	Ala 230	Gln	Arg	Thr	Leu	Glu 235	Lys	Met	Gly	Val	Asn 240	
gtt Val	cgc Arg	ctg Leu	aac Asn	gct Ala 245	atg Met	gtc Val	acc Thr	aac Asn	gtt Val 250	gac Asp	gct Ala	acc Thr	tcg Ser	gtc Val 255	acc Thr	768
tac Tyr	aag Lys	acc Thr	aag Lys 260	gac Asp	ggc Gly	gaa Glu	gag Glu	cac His 265	acc Thr	atc Ile	gaa Glu	tct Ser	ttc Phe 270	tgc Cys	aag Lys	816
att Ile	tgg Trp	tcc Ser 275	gct Ala	ggt Gly	gtt Val	gcg Ala	gca Ala 280	tcc Ser	cca Pro	ctg Leu	ggc Gly	aag Lys 285	ctc Leu	gtc Val	gca Ala	864
gag Glu	cag Gln 290	acc Thr	ggt Gly	gtt Val	gag Glu	acc Thr 295	gac Asp	cgc Arg	gca Ala	ggc Gly	cgc Arg 300	gtc Val	atg Met	gtt Val	aac Asn	912
gat Asp 305	gac Asp	ctg Leu	tct Ser	gtt Val	ggc Gly 310	gat Asp	cag Gln	aag Lys	aac Asn	gtc Val 315	ttc Phe	gtt Val	gtt Val	ggc Gly	gac Asp 320	960
atg 1008 Met	atg Met	aac Asn	tac Tyr	aac Asn 325	aac Asn	ctc Leu	cct Pro	ggt Gly	gtt Val 330	gct Ala	cag Gln	gta Val	gca Ala	atc Ile 335	cag Gln	
agt 1056 Ser	ggt Gly	gag Glu	tac Tyr 340	gtt Val	gct Ala	gag Glu	cag Gln	atc Ile 345	gaa Glu	gct Ala	gag Glu	gtt Val	gaa Glu 350	ggc Gly	cgc Arg	
tcc 1104 Ser	aac Asn	acc Thr 355	gag Glu	cgc Arg	gaa Glu	gct Ala	ttc Phe 360	gat Asp	tac Tyr	ttc Phe	gac Asp 365	aag Lys	ggc Gly	tcc Ser	atg Met	
gct 1152 Ala	acc Thr 370	att Ile	tcc Ser	cgc Arg	ttc Phe	tcc Ser 375	gca Ala	gtg Val	gtg Val	aag Lys	atg Met 380	ggc Gly	aag Lys	gtt Val	gag Glu	
gtc 1200 Val	acc Thr 385	ggc Gly	ttc Phe	atc Ile	ggt Gly 390	tgg Trp	gtt Val	ctg Leu	tgg Trp	ttg Leu 395	gct Ala	gtt Val	cac His	atc Ile	atg Met 400	
ttc 1248	ctg	gtt	ggc	ttc	cgc	aac	cgt	ttc	gtc	tcc	gca	atc	agc	tgg	ggc	

Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly  
405 410 415

ctg aac gca ctg tcc cgc aag cgt tgg aac ctg gca acc acc cgc cag  
1296

Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln  
420 425 430

cag ctc cac tca cgc acc acg ctg tcc aag ttc gct cac gag ctt gag  
1344

Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu  
435 440 445

gaa gca tct tct gat ctt cca atc gag ctg cgc gac aac cag cgt ttc  
1392

Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe  
450 455 460

agc gga aag taa  
1404

Ser Gly Lys  
465

<210> 4

<211> 467

<212> PRT

<213> Corynebacterium glutamicum ATCC13032

<400> 4

Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val  
1 5 10 15

Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala  
20 25 30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu  
35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly  
50 55 60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val  
65 70 75 80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr  
85 90 95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser  
100 105 110

Leu	Val	Val	Gly	Ala	Gly	Ala	Gly	Gln	Ser	Tyr	Phe	Gly	Asn	Asp	His	
		115					120					125				
Phe	Ala	Glu	Phe	Ala	Pro	Gly	Met	Lys	Ser	Ile	Asp	Asp	Ala	Leu	Glu	
	130					135					140					
Ile	Arg	Ala	Arg	Ile	Ile	Gly	Ala	Phe	Glu	Arg	Ala	Glu	Ile	Cys	Glu	
145					150					155					160	
Asp	Pro	Ala	Glu	Arg	Glu	Arg	Leu	Leu	Thr	Phe	Val	Val	Val	Gly	Ala	
				165					170					175		
Gly	Pro	Thr	Gly	Val	Glu	Leu	Ala	Gly	Gln	Leu	Ala	Glu	Met	Ala	His	
			180					185					190			
Arg	Thr	Leu	Ala	Gly	Glu	Tyr	Lys	Asn	Phe	Asn	Thr	Asn	Ser	Ala	Lys	
		195					200					205				
Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro	Phe	Gly	Lys	
	210					215					220					
Arg	Leu	Gly	Arg	Asn	Ala	Gln	Arg	Thr	Leu	Glu	Lys	Met	Gly	Val	Asn	
225					230					235					240	
Val	Arg	Leu	Asn	Ala	Met	Val	Thr	Asn	Val	Asp	Ala	Thr	Ser	Val	Thr	
				245					250					255		
Tyr	Lys	Thr	Lys	Asp	Gly	Glu	Glu	His	Thr	Ile	Glu	Ser	Phe	Cys	Lys	
			260					265					270			
Ile	Trp	Ser	Ala	Gly	Val	Ala	Ala	Ser	Pro	Leu	Gly	Lys	Leu	Val	Ala	
		275					280					285				
Glu	Gln	Thr	Gly	Val	Glu	Thr	Asp	Arg	Ala	Gly	Arg	Val	Met	Val	Asn	
	290					295					300					
Asp	Asp	Leu	Ser	Val	Gly	Asp	Gln	Lys	Asn	Val	Phe	Val	Val	Gly	Asp	
305					310					315					320	
Met	Met	Asn	Tyr	Asn	Asn	Leu	Pro	Gly	Val	Ala	Gln	Val	Ala	Ile	Gln	
				325					330					335		
Ser	Gly	Glu	Tyr	Val	Ala	Glu	Gln	Ile	Glu	Ala	Glu	Val	Glu	Gly	Arg	
			340					345					350			
Ser	Asn	Thr	Glu	Arg	Glu	Ala	Phe	Asp	Tyr	Phe	Asp	Lys	Gly	Ser	Met	
		355					360					365				
Ala	Thr	Ile	Ser	Arg	Phe	Ser	Ala	Val	Val	Lys	Met	Gly	Lys	Val	Glu	

370		375		380
Val Thr Gly Phe Ile Gly Trp Val Leu Trp Leu Ala Val His Ile Met				
385		390		395
Phe Leu Val Gly Phe Arg Asn Arg Phe Val Ser Ala Ile Ser Trp Gly				
	405		410	415
Leu Asn Ala Leu Ser Arg Lys Arg Trp Asn Leu Ala Thr Thr Arg Gln				
	420		425	430
Gln Leu His Ser Arg Thr Thr Leu Ser Lys Phe Ala His Glu Leu Glu				
	435		440	445
Glu Ala Ser Ser Asp Leu Pro Ile Glu Leu Arg Asp Asn Gln Arg Phe				
	450		455	460
Ser Gly Lys				
465				

<210> 5

<211> 1362

<212> DNA

<213> Corynebacterium diphtheriae

<220>

<221> CDS

<222>

<400> 5

atg act aac acc cca ttt cgc cca gaa ggt gga cgc cac cac gtt gta	48
Met Thr Asn Thr Pro Phe Arg Pro Glu Gly Gly Arg His His Val Val	
1 5 10 15	
gtt att ggc tcc ggc ttc ggt gga cta ttc gca gtt caa aac ctc aaa	96
Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Val Gln Asn Leu Lys	
20 25 30	
gat gca gat gtc gat atc acc ctc atc gac cgg aca aac cac cac ctt	144
Asp Ala Asp Val Asp Ile Thr Leu Ile Asp Arg Thr Asn His His Leu	
35 40 45	
ttc cag ccg ttg ctt tac caa gta gca acc ggt atc ttg tcg tct ggt	192
Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly	
50 55 60	
gaa atc gca cca caa acg cgt caa gtt ctt gca cag caa aat aat gtg	240
Glu Ile Ala Pro Gln Thr Arg Gln Val Leu Ala Gln Gln Asn Asn Val	
65 70 75 80	

cac His	gtt Val	ctt Leu	aag Lys	gct Ala 85	gaa Glu	gtc Val	acc Thr	gac Asp	att Ile 90	gac Asp	acc Thr	gaa Glu	tcg Ser	aag Lys 95	acg Thr	288
gtc Val	gtc Val	gca Ala	gac Asp 100	ttg Leu	gat Asp	gat Asp	tat Tyr	tct Ser 105	aaa Lys	aca Thr	att Ile	gaa Glu	tac Tyr 110	gat Asp	tcc Ser	336
ctg Leu	atc Ile	gtc Val 115	gcc Ala	gct Ala	ggg Gly	gca Ala	ggg Gly 120	cag Gln	tct Ser	tac Tyr	ttc Phe	gga Gly 125	aat Asn	gat Asp	cac His	384
ttc Phe	gcg Ala 130	gaa Glu	ttc Phe	gcg Ala	ccg Pro	ggg Gly 135	atg Met	aaa Lys	aca Thr	atc Ile	gat Asp 140	gat Asp	gca Ala	ctc Leu	gaa Glu	432
ctg Leu 145	cgt Arg	gcg Ala	cgc Arg	atc Ile	atc Ile 150	ggc Gly	gct Ala	ttc Phe	gaa Glu	cgc Arg 155	gca Ala	gaa Glu	atg Met	tgc Cys	gaa Glu 160	480
gat Asp	ccc Pro	aaa Lys	gaa Glu	cgt Arg 165	gaa Glu	cgc Arg	ctc Leu	ttg Leu	act Thr 170	ttt Phe	gtt Val	atc Ile	gtt Val	ggc Gly 175	gca Ala	528
gga Gly	cca Pro	aca Thr	ggc Gly 180	gta Val	gaa Glu	ctt Leu	gca Ala	ggg Gly 185	cag Gln	ctg Leu	gcc Ala	gaa Glu	atg Met 190	gca Ala	cac His	576
cgc Arg	acg Thr	ttg Leu 195	tct Ser	gga Gly	gag Glu	tac Tyr	acg Thr 200	cag Gln	ttc Phe	acg Thr	cct Pro	tcc Ser 205	aac Asn	gcg Ala	aag Lys	624
atc Ile 210	atc Ile	ctg Leu	ctt Leu	gac Asp	ggc Gly	gct Ala 215	cct Pro	cag Gln	gtg Val	ctt Leu	cca Pro 220	ccg Pro	ttc Phe	ggc Gly	aag Lys	672
cgt Arg 225	ttg Leu	ggg Gly	cgt Arg	act Thr	gca Ala 230	cag Gln	cgt Arg	gaa Glu	tta Leu	gaa Glu 235	aag Lys	att Ile	ggg Gly	gta Val	acg Thr 240	720
gtc Val	aag Lys	ctg Leu	aac Asn	gct Ala 245	atc Ile	gtt Val	acc Thr	ggc Gly	gta Val 250	gac Asp	gaa Glu	aac Asn	tca Ser	gtg Val 255	aca Thr	768
tat Tyr	aag Lys	tcc Ser	acc Thr 260	gtt Val	gat Asp	gat Asp	tct Ser	ttg Leu 265	cac His	acg Thr	atc Ile	gat Asp	tcc Ser 270	ttc Phe	tgc Cys	816



aag Lys	atc Ile	tgg Trp 275	tcg Ser	gca Ala	ggc Gly	gta Val	gcc Ala 280	gct Ala	tcc Ser	cca Pro	cta Leu	ggc Gly 285	aaa Lys	cta Leu	gtt Val	864
gca Ala	gag Glu 290	cag Gln	ctt Leu	ggt Gly	gtc Val	gag Glu 295	gtt Val	gat Asp	cgt Arg	gca Ala	gga Gly 300	cgc Arg	gtc Val	cca Pro	gtc Val	912
aac Asn 305	gaa Glu	gat Asp	ctt Leu	tct Ser	gtt Val 310	ggc Gly	gac Asp	gat Asp	aag Lys	aac Asn 315	gtc Val	ttt Phe	gtt Val	att Ile	ggc Gly 320	960
gat 1008 Asp	atg Met	atg Met	tcg Ser	ctc Leu 325	aac Asn	agg Arg	ctt Leu	ccg Pro	gga Gly 330	gtc Val	gca Ala	cag Gln	gta Val	gca Ala 335	atc Ile	
caa 1056 Gln	ggc Gly	ggt Gly	gaa Glu 340	tac Tyr	gtt Val	gct Ala	gag Glu 345	cag Gln	att Ile	gct Ala	gct Ala	ggg Gly 350	gtc Val	gag Glu	gga Gly	
cgt 1104 Arg	tcc Ser	tcg Ser 355	tct Ser	gaa Glu	cgc Arg	cca Pro	gcc Ala 360	ttt Phe	gaa Glu	tac Tyr	tac Tyr	gac Asp 365	aag Lys	ggt Gly	tcg Ser	
atg 1152 Met	gct Ala 370	acg Thr	gtg Val	tcg Ser	cgc Arg	ttt Phe 375	aac Asn	gcc Ala	gtt Val	gtg Val	aag Lys 380	ctt Leu	gga Gly	aaa Lys	gtt Val	
gaa 1200 Glu	gtt Val	acg Thr	gga Gly	ttt Phe	att Ile 390	ggc Gly	tgg Trp	gtc Val	atg Met	tgg Trp 395	ctt Leu	ctc Leu	gtc Val	cac His	ttg Leu 400	
atg 1248 Met	ttc Phe	ttg Leu	gtc Val	ggc Gly 405	ttc Phe	cgc Arg	aac Asn	cga Arg	gca Ala 410	act Thr	gcg Ala	gct Ala	ttc Phe	tct Ser 415	tgg Trp	
ggc 1296 Gly	atc Ile	aat Asn	gcg Ala 420	ctt Leu	tca Ser	cgt Arg	aag Lys	cgt Arg 425	tgg Trp	aac Asn	ctc Leu	gcc Ala	acc Thr 430	act Thr	cgt Arg	
cag 1344 Gln	cag Gln	ctt Leu	cac His	ggc Gly	cgt Arg	act Thr	ggt Gly	ttg Leu	caa Gln	aaa Lys	ctt Leu	act Thr	gcg Ala	ctc Leu	gtc Val	



435

440

445

1362

gat acc gcc gaa aag aag  
 Asp Thr Ala Glu Lys Lys  
 450

&lt;210&gt; 6

&lt;211&gt; 454

&lt;212&gt; PRT

&lt;213&gt; Corynebacterium diphtheriae

&lt;400&gt; 6

Met Thr Asn Thr Pro Phe Arg Pro Glu Gly Gly Arg His His Val Val  
 1 5 10 15

Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Val Gln Asn Leu Lys  
 20 25 30

Asp Ala Asp Val Asp Ile Thr Leu Ile Asp Arg Thr Asn His His Leu  
 35 40 45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly  
 50 55 60

Glu Ile Ala Pro Gln Thr Arg Gln Val Leu Ala Gln Gln Asn Asn Val  
 65 70 75 80

His Val Leu Lys Ala Glu Val Thr Asp Ile Asp Thr Glu Ser Lys Thr  
 85 90 95

Val Val Ala Asp Leu Asp Asp Tyr Ser Lys Thr Ile Glu Tyr Asp Ser  
 100 105 110

Leu Ile Val Ala Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His  
 115 120 125

Phe Ala Glu Phe Ala Pro Gly Met Lys Thr Ile Asp Asp Ala Leu Glu  
 130 135 140

Leu Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Met Cys Glu  
 145 150 155 160

Asp Pro Lys Glu Arg Glu Arg Leu Leu Thr Phe Val Ile Val Gly Ala  
 165 170 175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His  
 180 185 190

Arg Thr Leu Ser Gly Glu Tyr Thr Gln Phe Thr Pro Ser Asn Ala Lys  
 195 200 205

Ile	Ile	Leu	Leu	Asp	Gly	Ala	Pro	Gln	Val	Leu	Pro	Pro	Phe	Gly	Lys
	210					215					220				
Arg	Leu	Gly	Arg	Thr	Ala	Gln	Arg	Glu	Leu	Glu	Lys	Ile	Gly	Val	Thr
225					230					235					240
Val	Lys	Leu	Asn	Ala	Ile	Val	Thr	Gly	Val	Asp	Glu	Asn	Ser	Val	Thr
				245					250					255	
Tyr	Lys	Ser	Thr	Val	Asp	Asp	Ser	Leu	His	Thr	Ile	Asp	Ser	Phe	Cys
			260					265					270		
Lys	Ile	Trp	Ser	Ala	Gly	Val	Ala	Ala	Ser	Pro	Leu	Gly	Lys	Leu	Val
		275					280					285			
Ala	Glu	Gln	Leu	Gly	Val	Glu	Val	Asp	Arg	Ala	Gly	Arg	Val	Pro	Val
	290					295					300				
Asn	Glu	Asp	Leu	Ser	Val	Gly	Asp	Asp	Lys	Asn	Val	Phe	Val	Ile	Gly
305					310					315					320
Asp	Met	Met	Ser	Leu	Asn	Arg	Leu	Pro	Gly	Val	Ala	Gln	Val	Ala	Ile
				325					330					335	
Gln	Gly	Gly	Glu	Tyr	Val	Ala	Glu	Gln	Ile	Ala	Ala	Gly	Val	Glu	Gly
			340					345					350		
Arg	Ser	Ser	Ser	Glu	Arg	Pro	Ala	Phe	Glu	Tyr	Tyr	Asp	Lys	Gly	Ser
		355					360					365			
Met	Ala	Thr	Val	Ser	Arg	Phe	Asn	Ala	Val	Val	Lys	Leu	Gly	Lys	Val
	370					375					380				
Glu	Val	Thr	Gly	Phe	Ile	Gly	Trp	Val	Met	Trp	Leu	Leu	Val	His	Leu
385					390					395					400
Met	Phe	Leu	Val	Gly	Phe	Arg	Asn	Arg	Ala	Thr	Ala	Ala	Phe	Ser	Trp
				405					410					415	
Gly	Ile	Asn	Ala	Leu	Ser	Arg	Lys	Arg	Trp	Asn	Leu	Ala	Thr	Thr	Arg
			420					425					430		
Gln	Gln	Leu	His	Gly	Arg	Thr	Gly	Leu	Gln	Lys	Leu	Thr	Ala	Leu	Val
		435					440					445			
Asp	Thr	Ala	Glu	Lys	Lys										
	450														

<211> 1302  
 <212> DNA  
 <213> Escherichia coli

<220>  
 <221> CDS  
 <222>

<400> 7

ttg	act	acg	cca	ttg	aaa	aag	att	gtg	att	gtc	ggc	ggc	ggt	gct	ggt	48
Met	Thr	Thr	Pro	Leu	Lys	Lys	Ile	Val	Ile	Val	Gly	Gly	Gly	Ala	Gly	
1				5				10						15		
ggg	ctg	gaa	atg	gca	aca	cag	ctg	ggg	cat	aag	ctg	gga	cgc	aag	aaa	96
Gly	Leu	Glu	Met	Ala	Thr	Gln	Leu	Gly	His	Lys	Leu	Gly	Arg	Lys	Lys	
			20					25					30			
aaa	gcc	aaa	att	acg	ctg	gtc	gat	cgt	aac	cac	agc	cac	ctg	tgg	aaa	144
Lys	Ala	Lys	Ile	Thr	Leu	Val	Asp	Arg	Asn	His	Ser	His	Leu	Trp	Lys	
		35					40					45				
ccg	ctg	ctg	cac	gaa	gtg	gcg	act	ggc	tcg	ctt	gat	gaa	ggc	gtc	gat	192
Pro	Leu	Leu	His	Glu	Val	Ala	Thr	Gly	Ser	Leu	Asp	Glu	Gly	Val	Asp	
	50					55					60					
gcg	ttg	agc	tat	ctg	gcc	cat	gcg	cgc	aat	cat	ggt	ttc	cag	ttc	cag	240
Ala	Leu	Ser	Tyr	Leu	Ala	His	Ala	Arg	Asn	His	Gly	Phe	Gln	Phe	Gln	
65					70					75					80	
ctg	ggt	tcc	gtc	att	gat	att	gat	cgt	gaa	gcg	aaa	aca	atc	act	att	288
Leu	Gly	Ser	Val	Ile	Asp	Ile	Asp	Arg	Glu	Ala	Lys	Thr	Ile	Thr	Ile	
				85					90					95		
gca	gaa	ctg	cgc	gac	gag	aaa	ggt	gaa	ctg	ctg	gtt	ccg	gaa	cgt	aaa	336
Ala	Glu	Leu	Arg	Asp	Glu	Lys	Gly	Glu	Leu	Leu	Val	Pro	Glu	Arg	Lys	
			100					105					110			
atc	gcc	tat	gac	acc	ctg	gta	atg	gcg	ctg	ggt	agc	acc	tct	aac	gat	384
Ile	Ala	Tyr	Asp	Thr	Leu	Val	Met	Ala	Leu	Gly	Ser	Thr	Ser	Asn	Asp	
		115					120					125				
ttc	aat	acg	cca	ggt	gtc	aaa	gag	aac	tgc	att	ttc	ctc	gat	aac	ccg	432
Phe	Asn	Thr	Pro	Gly	Val	Lys	Glu	Asn	Cys	Ile	Phe	Leu	Asp	Asn	Pro	
	130					135					140					
cac	cag	gcg	cgt	cgc	ttc	cac	cag	gag	atg	ctg	aat	ttg	ttc	ctg	aaa	480
His	Gln	Ala	Arg	Arg	Phe	His	Gln	Glu	Met	Leu	Asn	Leu	Phe	Leu	Lys	
145					150					155					160	

tac	tcc	gcc	aac	ctg	ggc	gcg	aat	ggc	aaa	gtg	aac	att	gcg	att	gtc	528
Tyr	Ser	Ala	Asn	Leu	Gly	Ala	Asn	Gly	Lys	Val	Asn	Ile	Ala	Ile	Val	
				165					170					175		
ggc	ggc	ggc	gcg	acg	ggt	gta	gaa	ctc	tcc	gct	gaa	ttg	cac	aac	gcg	576
Gly	Gly	Gly	Ala	Thr	Gly	Val	Glu	Leu	Ser	Ala	Glu	Leu	His	Asn	Ala	
			180					185					190			
gtc	aag	caa	ctg	cac	agc	tac	ggt	tac	aaa	ggc	ctg	acc	aac	gaa	gcc	624
Val	Lys	Gln	Leu	His	Ser	Tyr	Gly	Tyr	Lys	Gly	Leu	Thr	Asn	Glu	Ala	
		195					200					205				
ctg	aac	gta	acg	ctg	gta	gaa	gcg	gga	gaa	cgt	att	ttg	cct	gcg	tta	672
Leu	Asn	Val	Thr	Leu	Val	Glu	Ala	Gly	Glu	Arg	Ile	Leu	Pro	Ala	Leu	
	210					215					220					
ccg	cca	cgt	atc	tct	gct	gcg	gcc	cac	aac	gag	cta	acg	aaa	ctt	ggc	720
Pro	Pro	Arg	Ile	Ser	Ala	Ala	Ala	His	Asn	Glu	Leu	Thr	Lys	Leu	Gly	
225					230					235					240	
gtt	cgc	gtg	ctg	acg	caa	acc	atg	gtc	acc	agt	gct	gat	gaa	ggc	ggc	768
Val	Arg	Val	Leu	Thr	Gln	Thr	Met	Val	Thr	Ser	Ala	Asp	Glu	Gly	Gly	
				245					250					255		
ctg	cac	act	aaa	gat	ggc	gaa	tat	att	gag	gct	gat	ctg	atg	gta	tgg	816
Leu	His	Thr	Lys	Asp	Gly	Glu	Tyr	Ile	Glu	Ala	Asp	Leu	Met	Val	Trp	
			260					265					270			
gca	gcc	ggg	atc	aaa	gcg	cca	gac	ttc	ctg	aaa	gat	atc	ggt	ggt	ctt	864
Ala	Ala	Gly	Ile	Lys	Ala	Pro	Asp	Phe	Leu	Lys	Asp	Ile	Gly	Gly	Leu	
		275					280					285				
gaa	act	aac	cgt	atc	aac	cag	ctg	gtg	gtg	gaa	ccg	acg	ctg	caa	acc	912
Glu	Thr	Asn	Arg	Ile	Asn	Gln	Leu	Val	Val	Glu	Pro	Thr	Leu	Gln	Thr	
	290					295					300					
acc	cgc	gat	cca	gac	att	tac	gct	att	ggc	gac	tgc	gcg	tca	tgc	ccg	960
Thr	Arg	Asp	Pro	Asp	Ile	Tyr	Ala	Ile	Gly	Asp	Cys	Ala	Ser	Cys	Pro	
305					310					315					320	
cgt	ccg	gaa	ggg	ggc	ttt	gtt	ccg	ccg	cgt	gct	cag	gct	gca	cac	cag	
1008																
Arg	Pro	Glu	Gly	Gly	Phe	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln	
				325					330					335		
atg	gcg	act	tgc	gca	atg	aac	aac	att	ctg	gcg	cag	atg	aac	ggt	aag	
1056																
Met	Ala	Thr	Cys	Ala	Met	Asn	Asn	Ile	Leu	Ala	Gln	Met	Asn	Gly	Lys	
			340					345					350			

ccg ctg aaa aat tat cag tat aaa gat cat ggt tcg ctg gta tcg ctg  
 1104  
 Pro Leu Lys Asn Tyr Gln Tyr Lys Asp His Gly Ser Leu Val Ser Leu  
 355 360 365

tcg aac ttc tcc acc gtc ggt agc ctg atg ggt aac ctg acg cgc ggc  
 1152  
 Ser Asn Phe Ser Thr Val Gly Ser Leu Met Gly Asn Leu Thr Arg Gly  
 370 375 380

tca atg atg att gaa gga cga att gcg cgc ttt gta tat atc tcg cta  
 1200  
 Ser Met Met Ile Glu Gly Arg Ile Ala Arg Phe Val Tyr Ile Ser Leu  
 385 390 395 400

tac cga atg cat cag att gcg ctg cat ggt tac ttt aaa acc gga tta  
 1248  
 Tyr Arg Met His Gln Ile Ala Leu His Gly Tyr Phe Lys Thr Gly Leu  
 405 410 415

atg atg ctg gtg ggg agt att aac cgc gtt atc cgt ccg cgt ttg aag  
 1296  
 Met Met Leu Val Gly Ser Ile Asn Arg Val Ile Arg Pro Arg Leu Lys  
 420 425 430

ttg cat  
 Leu His 1302

<210> 8  
 <211> 434  
 <212> PRT  
 <213> Escherichia coli

<400> 8  
 Met Thr Thr Pro Leu Lys Lys Ile Val Ile Val Gly Gly Gly Ala Gly  
 1 5 10 15

Gly Leu Glu Met Ala Thr Gln Leu Gly His Lys Leu Gly Arg Lys Lys  
 20 25 30

Lys Ala Lys Ile Thr Leu Val Asp Arg Asn His Ser His Leu Trp Lys  
 35 40 45

Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp  
 50 55 60

Ala Leu Ser Tyr Leu Ala His Ala Arg Asn His Gly Phe Gln Phe Gln  
 65 70 75 80

Leu Gly Ser Val Ile Asp Ile Asp Arg Glu Ala Lys Thr Ile Thr Ile

85							90					95			
Ala	Glu	Leu	Arg 100	Asp	Glu	Lys	Gly	Glu 105	Leu	Leu	Val	Pro	Glu 110	Arg	Lys
Ile	Ala	Tyr 115	Asp	Thr	Leu	Val	Met 120	Ala	Leu	Gly	Ser	Thr 125	Ser	Asn	Asp
Phe	Asn 130	Thr	Pro	Gly	Val	Lys 135	Glu	Asn	Cys	Ile	Phe 140	Leu	Asp	Asn	Pro
His 145	Gln	Ala	Arg	Arg	Phe 150	His	Gln	Glu	Met	Leu 155	Asn	Leu	Phe	Leu	Lys 160
Tyr	Ser	Ala	Asn 165	Leu	Gly	Ala	Asn	Gly	Lys 170	Val	Asn	Ile	Ala	Ile 175	Val
Gly	Gly	Gly	Ala 180	Thr	Gly	Val	Glu	Leu 185	Ser	Ala	Glu	Leu	His 190	Asn	Ala
Val	Lys	Gln 195	Leu	His	Ser	Tyr	Gly 200	Tyr	Lys	Gly	Leu	Thr 205	Asn	Glu	Ala
Leu	Asn 210	Val	Thr	Leu	Val	Glu 215	Ala	Gly	Glu	Arg	Ile 220	Leu	Pro	Ala	Leu
Pro 225	Pro	Arg	Ile	Ser	Ala 230	Ala	Ala	His	Asn	Glu 235	Leu	Thr	Lys	Leu	Gly 240
Val	Arg	Val	Leu	Thr 245	Gln	Thr	Met	Val	Thr 250	Ser	Ala	Asp	Glu	Gly 255	Gly
Leu	His	Thr	Lys 260	Asp	Gly	Glu	Tyr	Ile 265	Glu	Ala	Asp	Leu	Met 270	Val	Trp
Ala	Ala	Gly 275	Ile	Lys	Ala	Pro	Asp 280	Phe	Leu	Lys	Asp	Ile 285	Gly	Gly	Leu
Glu	Thr 290	Asn	Arg	Ile	Asn	Gln 295	Leu	Val	Val	Glu	Pro 300	Thr	Leu	Gln	Thr
Thr 305	Arg	Asp	Pro	Asp	Ile 310	Tyr	Ala	Ile	Gly	Asp 315	Cys	Ala	Ser	Cys	Pro 320
Arg	Pro	Glu	Gly	Gly 325	Phe	Val	Pro	Pro	Arg 330	Ala	Gln	Ala	Ala	His 335	Gln
Met	Ala	Thr	Cys 340	Ala	Met	Asn	Asn	Ile 345	Leu	Ala	Gln	Met	Asn 350	Gly	Lys

Pro	Leu	Lys	Asn	Tyr	Gln	Tyr	Lys	Asp	His	Gly	Ser	Leu	Val	Ser	Leu
		355					360					365			
Ser	Asn	Phe	Ser	Thr	Val	Gly	Ser	Leu	Met	Gly	Asn	Leu	Thr	Arg	Gly
	370					375					380				
Ser	Met	Met	Ile	Glu	Gly	Arg	Ile	Ala	Arg	Phe	Val	Tyr	Ile	Ser	Leu
385					390					395					400
Tyr	Arg	Met	His	Gln	Ile	Ala	Leu	His	Gly	Tyr	Phe	Lys	Thr	Gly	Leu
				405					410					415	
Met	Met	Leu	Val	Gly	Ser	Ile	Asn	Arg	Val	Ile	Arg	Pro	Arg	Leu	Lys
			420					425					430		

Leu His

<210> 9

<211> 1296

<212> DNA

<213> *Pseudomonas fluorescens*

<220>

<221> CDS

<222>

<400> 9

atg	act	cat	cgt	att	gtc	atc	gtt	ggc	ggc	ggc	gcc	ggc	ggt	ctg	gag	48
Met	Thr	His	Arg	Ile	Val	Ile	Val	Gly	Gly	Gly	Ala	Gly	Gly	Leu	Glu	
1				5				10						15		
ttg	gct	acc	cgt	ctg	ggt	aag	act	ctg	ggc	aag	cgt	ggc	acg	gcc	agt	96
Leu	Ala	Thr	Arg	Leu	Gly	Lys	Thr	Leu	Gly	Lys	Arg	Gly	Thr	Ala	Ser	
			20					25					30			
gtg	atg	ctg	gtc	gac	gcg	aac	ctg	acc	cac	atc	tgg	aaa	ccg	cta	ctg	144
Val	Met	Leu	Val	Asp	Ala	Asn	Leu	Thr	His	Ile	Trp	Lys	Pro	Leu	Leu	
		35					40					45				
cac	gaa	gtg	gcc	gcc	ggc	tcc	ttg	aac	tcc	tcc	gaa	gac	gaa	ctc	aac	192
His	Glu	Val	Ala	Ala	Gly	Ser	Leu	Asn	Ser	Ser	Glu	Asp	Glu	Leu	Asn	
	50					55					60					
tat	gtc	gcc	cag	gca	aaa	tgg	aac	cac	ttc	gag	ttc	cag	ctc	ggg	cgc	240
Tyr	Val	Ala	Gln	Ala	Lys	Trp	Asn	His	Phe	Glu	Phe	Gln	Leu	Gly	Arg	
65					70					75					80	
atg	agc	ggc	ctg	gat	cgc	gag	cgc	aag	aga	atc	caa	ctg	gcc	gcc	acc	288
Met	Ser	Gly	Leu	Asp	Arg	Glu	Arg	Lys	Arg	Ile	Gln	Leu	Ala	Ala	Thr	



85								90				95				
tat	gac	gag	acc	ggc	gtc	gag	ctg	ttg	ccg	gcc	cgg	gaa	ctg	ggc	tac	336
Tyr	Asp	Glu	Thr	Gly	Val	Glu	Leu	Leu	Pro	Ala	Arg	Glu	Leu	Gly	Tyr	
			100					105					110			
gac	acc	ctg	gtg	att	gcc	gtc	ggc	agc	acc	acc	aat	gac	ttc	ggc	acc	384
Asp	Thr	Leu	Val	Ile	Ala	Val	Gly	Ser	Thr	Thr	Asn	Asp	Phe	Gly	Thr	
		115					120					125				
gaa	ggc	gcg	gcg	cag	cac	tgc	ctg	ttc	ctc	gac	acc	cgc	aaa	cag	gcc	432
Glu	Gly	Ala	Ala	Gln	His	Cys	Leu	Phe	Leu	Asp	Thr	Arg	Lys	Gln	Ala	
	130					135					140					
gag	cgc	ttc	cat	cag	caa	ttg	ctg	cac	cac	tat	ctg	cgc	gcc	cac	gcc	480
Glu	Arg	Phe	His	Gln	Gln	Leu	Leu	His	His	Tyr	Leu	Arg	Ala	His	Ala	
145					150					155					160	
ggg	cag	acc	gat	atc	gtc	gag	cgc	atc	agc	gtc	gcc	att	gtc	ggc	gcc	528
Gly	Gln	Thr	Asp	Ile	Val	Glu	Arg	Ile	Ser	Val	Ala	Ile	Val	Gly	Ala	
				165					170					175		
ggt	gcg	acc	ggg	gtc	gaa	ctg	gcc	gcc	gag	ctg	cat	aat	gcc	gcc	cac	576
Gly	Ala	Thr	Gly	Val	Glu	Leu	Ala	Ala	Glu	Leu	His	Asn	Ala	Ala	His	
			180					185					190			
gaa	ctg	cac	gcc	tac	ggc	ctg	gac	cgg	atc	aaa	ccg	gag	aac	atg	cac	624
Glu	Leu	His	Ala	Tyr	Gly	Leu	Asp	Arg	Ile	Lys	Pro	Glu	Asn	Met	His	
		195					200					205				
atc	acc	ctg	atc	gag	gcc	ggg	cca	cgc	gtc	ttg	ccg	gcc	ctg	ccg	gag	672
Ile	Thr	Leu	Ile	Glu	Ala	Gly	Pro	Arg	Val	Leu	Pro	Ala	Leu	Pro	Glu	
	210					215					220					
cgt	atc	ggc	ggg	ccg	gtg	cac	aag	acc	ctg	gaa	aaa	ctc	ggg	gtc	aac	720
Arg	Ile	Gly	Gly	Pro	Val	His	Lys	Thr	Leu	Glu	Lys	Leu	Gly	Val	Asn	
225					230					235					240	
gtc	atg	acc	aac	gcc	gcc	gtc	agc	cag	gtg	acc	gcc	gac	agc	ctg	att	768
Val	Met	Thr	Asn	Ala	Ala	Val	Ser	Gln	Val	Thr	Ala	Asp	Ser	Leu	Ile	
				245					250					255		
acc	gcg	gac	ggc	aaa	gtg	atc	gac	gcg	agc	ctg	aaa	gtc	tgg	gcc	gcc	816
Thr	Ala	Asp	Gly	Lys	Val	Ile	Asp	Ala	Ser	Leu	Lys	Val	Trp	Ala	Ala	
			260					265					270			
ggg	att	cgc	gcc	ccg	gac	ttc	ctc	aag	gac	atc	gac	ggg	ctg	gag	acc	864
Gly	Ile	Arg	Ala	Pro	Asp	Phe	Leu	Lys	Asp	Ile	Asp	Gly	Leu	Glu	Thr	
		275					280					285				

aac	cgg	atc	aac	cag	ttg	cac	gtg	ctg	ccc	act	ttg	cag	acc	acc	cgc	912
Asn	Arg	Ile	Asn	Gln	Leu	His	Val	Leu	Pro	Thr	Leu	Gln	Thr	Thr	Arg	
	290					295					300					

gac	gag	aac	atc	ttc	gcc	ttc	ggc	gac	tgc	gcc	gcc	tgc	ccg	caa	ccc	960
Asp	Glu	Asn	Ile	Phe	Ala	Phe	Gly	Asp	Cys	Ala	Ala	Cys	Pro	Gln	Pro	
305					310					315					320	

ggc	agc	gag	cgc	aac	gtc	cca	cct	cgc	gcc	cag	gcc	gca	cac	cag	caa	
1008																
Gly	Ser	Glu	Arg	Asn	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln	Gln	
				325					330					335		

gcc	tca	ctg	ctg	gcc	aaa	tcc	ttg	aag	ctg	cgg	atc	gag	ggc	aag	gcc	
1056																
Ala	Ser	Leu	Leu	Ala	Lys	Ser	Leu	Lys	Leu	Arg	Ile	Glu	Gly	Lys	Ala	
			340					345					350			

ctg	ccg	gaa	tac	aaa	tac	acc	gac	tac	ggc	tcg	ctg	atc	tcg	ctg	tcg	
1104																
Leu	Pro	Glu	Tyr	Lys	Tyr	Thr	Asp	Tyr	Gly	Ser	Leu	Ile	Ser	Leu	Ser	
		355					360					365				

cgg	ttc	tcg	gca	gtg	ggc	aac	ctg	atg	ggt	aac	ctg	acc	ggc	agc	gtg	
1152																
Arg	Phe	Ser	Ala	Val	Gly	Asn	Leu	Met	Gly	Asn	Leu	Thr	Gly	Ser	Val	
	370					375					380					

atg	ctc	gaa	ggc	tgg	ctg	gcg	cgg	atg	ttc	tat	gtg	tcg	ctg	tac	cgc	
1200																
Met	Leu	Glu	Gly	Trp	Leu	Ala	Arg	Met	Phe	Tyr	Val	Ser	Leu	Tyr	Arg	
385					390					395					400	

atg	cac	cag	atg	gcg	ctg	tac	ggc	atg	ttc	cgc	acg	gcc	atg	ttg	atg	
1248																
Met	His	Gln	Met	Ala	Leu	Tyr	Gly	Met	Phe	Arg	Thr	Ala	Met	Leu	Met	
				405					410					415		

ctg	ggt	agc	aag	atc	ggg	cgt	ggg	acc	gag	cct	cgg	ctg	aag	ctg	cac	
1296																
Leu	Gly	Ser	Lys	Ile	Gly	Arg	Gly	Thr	Glu	Pro	Arg	Leu	Lys	Leu	His	
			420					425					430			

<210> 10  
 <211> 432  
 <212> PRT  
 <213> Pseudomonas fluorescens

<400>	10															
Met	Thr	His	Arg	Ile	Val	Ile	Val	Gly	Gly	Gly	Ala	Gly	Gly	Leu	Glu	

1				5					10					15		
Leu	Ala	Thr	Arg 20	Leu	Gly	Lys	Thr	Leu 25	Gly	Lys	Arg	Gly	Thr 30	Ala	Ser	
Val	Met	Leu 35	Val	Asp	Ala	Asn	Leu 40	Thr	His	Ile	Trp	Lys 45	Pro	Leu	Leu	
His	Glu 50	Val	Ala	Ala	Gly	Ser 55	Leu	Asn	Ser	Ser	Glu 60	Asp	Glu	Leu	Asn	
Tyr 65	Val	Ala	Gln	Ala	Lys 70	Trp	Asn	His	Phe	Glu 75	Phe	Gln	Leu	Gly	Arg 80	
Met	Ser	Gly	Leu	Asp 85	Arg	Glu	Arg	Lys	Arg 90	Ile	Gln	Leu	Ala	Ala 95	Thr	
Tyr	Asp	Glu	Thr 100	Gly	Val	Glu	Leu	Leu 105	Pro	Ala	Arg	Glu	Leu 110	Gly	Tyr	
Asp	Thr	Leu 115	Val	Ile	Ala	Val	Gly 120	Ser	Thr	Thr	Asn	Asp 125	Phe	Gly	Thr	
Glu	Gly 130	Ala	Ala	Gln	His	Cys 135	Leu	Phe	Leu	Asp	Thr 140	Arg	Lys	Gln	Ala	
Glu 145	Arg	Phe	His	Gln	Gln 150	Leu	Leu	His	His	Tyr 155	Leu	Arg	Ala	His	Ala 160	
Gly	Gln	Thr	Asp	Ile 165	Val	Glu	Arg	Ile	Ser 170	Val	Ala	Ile	Val	Gly 175	Ala	
Gly	Ala	Thr	Gly 180	Val	Glu	Leu	Ala	Ala 185	Glu	Leu	His	Asn	Ala 190	Ala	His	
Glu	Leu	His 195	Ala	Tyr	Gly	Leu	Asp 200	Arg	Ile	Lys	Pro	Glu 205	Asn	Met	His	
Ile	Thr 210	Leu	Ile	Glu	Ala	Gly 215	Pro	Arg	Val	Leu	Pro 220	Ala	Leu	Pro	Glu	
Arg 225	Ile	Gly	Gly	Pro	Val 230	His	Lys	Thr	Leu	Glu 235	Lys	Leu	Gly	Val	Asn 240	
Val	Met	Thr	Asn	Ala 245	Ala	Val	Ser	Gln	Val 250	Thr	Ala	Asp	Ser	Leu 255	Ile	
Thr	Ala	Asp	Gly 260	Lys	Val	Ile	Asp	Ala 265	Ser	Leu	Lys	Val	Trp 270	Ala	Ala	

Gly	Ile	Arg	Ala	Pro	Asp	Phe	Leu	Lys	Asp	Ile	Asp	Gly	Leu	Glu	Thr	
		275					280					285				
Asn	Arg	Ile	Asn	Gln	Leu	His	Val	Leu	Pro	Thr	Leu	Gln	Thr	Thr	Arg	
	290					295					300					
Asp	Glu	Asn	Ile	Phe	Ala	Phe	Gly	Asp	Cys	Ala	Ala	Cys	Pro	Gln	Pro	
305					310					315					320	
Gly	Ser	Glu	Arg	Asn	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln	Gln	
				325					330					335		
Ala	Ser	Leu	Leu	Ala	Lys	Ser	Leu	Lys	Leu	Arg	Ile	Glu	Gly	Lys	Ala	
			340					345					350			
Leu	Pro	Glu	Tyr	Lys	Tyr	Thr	Asp	Tyr	Gly	Ser	Leu	Ile	Ser	Leu	Ser	
		355					360					365				
Arg	Phe	Ser	Ala	Val	Gly	Asn	Leu	Met	Gly	Asn	Leu	Thr	Gly	Ser	Val	
	370					375					380					
Met	Leu	Glu	Gly	Trp	Leu	Ala	Arg	Met	Phe	Tyr	Val	Ser	Leu	Tyr	Arg	
385					390					395					400	
Met	His	Gln	Met	Ala	Leu	Tyr	Gly	Met	Phe	Arg	Thr	Ala	Met	Leu	Met	
				405					410					415		
Leu	Gly	Ser	Lys	Ile	Gly	Arg	Gly	Thr	Glu	Pro	Arg	Leu	Lys	Leu	His	
			420					425					430			

<210> 11  
 <211> 1296  
 <212> DNA  
 <213> Azotobacter vinelandii

<220>  
 <221> CDS  
 <222>

<400> 11																	
atg	act	cat	cgt	atc	gta	atc	gtc	ggc	ggt	ggc	gct	ggc	ggc	gtg	gaa		48
Met	Thr	His	Arg	Ile	Val	Ile	Val	Gly	Gly	Gly	Ala	Gly	Gly	Val	Glu		
1				5				10						15			
ctc	gct	acc	cgc	ctc	ggc	aag	acc	atg	ggc	agg	aac	ttc	cag	gcg	aag		96
Leu	Ala	Thr	Arg	Leu	Gly	Lys	Thr	Met	Gly	Arg	Asn	Phe	Gln	Ala	Lys		
			20					25					30				
atc	acc	ctg	gtc	gac	gcc	aac	atg	acc	cac	ctg	tgg	aaa	ccg	ctg	ctg		144
Ile	Thr	Leu	Val	Asp	Ala	Asn	Met	Thr	His	Leu	Trp	Lys	Pro	Leu	Leu		

35						40					45						
cac His	gaa Glu 50	gtc Val	gcc Ala	gcc Ala	ggc Gly	tcg Ser 55	ctg Leu	aac Asn	tcg Ser	acc Thr	ggc Gly 60	gac Asp	gaa Glu	ctg Leu	aac Asn	192	
tat Tyr 65	gtg Val	gcc Ala	cag Gln	gcc Ala	aaa Lys 70	tgg Trp	aac Asn	aac Asn	ttc Phe	gag Glu 75	ttc Phe	cag Gln	tac Tyr	ggc Gly	cgc Arg 80	240	
atg Met	tgc Cys	ggt Gly	ctg Leu	gac Asp 85	cgg Arg	gcc Ala	aac Asn	aag Lys	cgt Arg 90	atc Ile	cgc Arg	ctg Leu	gcg Ala	gcc Ala 95	cag Gln	288	
ccg Pro	gcc Ala	cag Gln	gaa Glu 100	gat Asp	cgc Arg	gcg Ala	ccc Pro	ctg Leu 105	ccc Pro	gag Glu	cgc Arg	gaa Glu	ctg Leu 110	gaa Glu	tac Tyr	336	
gac Asp	acc Thr	ctg Leu 115	gtc Val	ctt Leu	tcc Ser	gtc Val	ggc Gly 120	agc Ser	acc Thr	acc Thr	aat Asn	gac Asp 125	ttc Phe	ggc Gly	acc Thr	384	
ccg Pro 130	ggc Gly	gcc Ala	gcc Ala	gag Glu	aac Asn	tgt Cys 135	att Ile	ttc Phe	ctg Leu	gaa Glu	ggc Gly 140	cgc Arg	gac Asp	cag Gln	gcc Ala	432	
gag Glu 145	cgt Arg	ttc Phe	cgc Arg	cgt Arg	ccg Pro 150	ctg Leu	ctc Leu	agc Ser	cac His	tac Tyr 155	ttg Leu	cgt Arg	gcc Ala	cac His	gcc Ala 160	480	
agc Ser	aat Asn	gac Asp	gac Asp	ggc Gly 165	cat His	cag Gln	gtc Val	aag Lys	gtc Val 170	gcc Ala	atc Ile	gtc Val	ggc Gly	gcc Ala 175	ggt Gly	528	
gcc Ala	acc Thr	ggg Gly	gtc Val 180	gaa Glu	ctg Leu	gcc Ala	gca Ala	gaa Glu 185	ctg Leu	cgc Arg	cac His	gcc Ala	tcc Ser 190	aag Lys	gaa Glu	576	
ctg Leu	gtc Val	gcc Ala 195	tat Tyr	ggg Gly	ctg Leu	gag Glu	cgc Arg 200	att Ile	ccg Pro	ccg Pro	gag Glu	aac Asn 205	ctc Leu	agc Ser	atc Ile	624	
acg Thr 210	ctg Leu	atc Ile	gaa Glu	tcc Ser	agc Ser	ccg Pro 215	cgt Arg	gta Val	ctc Leu	gcc Ala	gcc Ala 220	ctg Leu	ccc Pro	gaa Glu	cgc Arg	672	
atc Ile 225	agc Ser	cgc Arg	tcc Ser	gcg Ala	cac His 230	gcc Ala	acc Thr	ctg Leu	gaa Glu	agc Ser 235	ctg Leu	ggc Gly	gtt Val	cgc Arg	gtg Val 240	720	

ctc	gtc	agc	acc	gcc	gtc	agc	gag	gtc	acc	gcg	gaa	ggc	gtg	aag	acg	768
Leu	Val	Ser	Thr	Ala	Val	Ser	Glu	Val	Thr	Ala	Glu	Gly	Val	Lys	Thr	
				245					250					255		
aag	gac	gac	cag	ttc	atc	ccc	gcc	gac	ctc	atg	gtc	tgg	gcc	gca	ggc	816
Lys	Asp	Asp	Gln	Phe	Ile	Pro	Ala	Asp	Leu	Met	Val	Trp	Ala	Ala	Gly	
			260					265					270			
gtc	cgc	gcg	ccc	gcc	ttc	ctc	aag	gag	ctg	gat	ggc	ctg	gaa	acc	aat	864
Val	Arg	Ala	Pro	Ala	Phe	Leu	Lys	Glu	Leu	Asp	Gly	Leu	Glu	Thr	Asn	
		275					280					285				
cgc	atc	aac	cag	ttg	cag	gtc	cgc	cag	acc	ctg	cag	act	act	ctg	gac	912
Arg	Ile	Asn	Gln	Leu	Gln	Val	Arg	Gln	Thr	Leu	Gln	Thr	Thr	Leu	Asp	
	290					295					300					
gac	gat	atc	ttc	gcc	ttc	ggc	gat	tgt	gcc	tcc	tgc	ccg	cag	ccg	ggc	960
Asp	Asp	Ile	Phe	Ala	Phe	Gly	Asp	Cys	Ala	Ser	Cys	Pro	Gln	Pro	Gly	
305					310					315					320	
acc	gac	cgc	ccc	gtt	ccg	ccg	cgc	gcc	cag	gcc	gct	cac	cag	cag	gcc	
1008																
Thr	Asp	Arg	Pro	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln	Gln	Ala	
				325					330					335		
agc	ctg	ctg	gcc	aag	tcg	ctc	cac	cgc	aag	ctg	cag	gaa	gac	agc	ctc	
1056																
Ser	Leu	Leu	Ala	Lys	Ser	Leu	His	Arg	Lys	Leu	Gln	Glu	Asp	Ser	Leu	
			340					345					350			
tgc	tgg	agt	atc	gct	aca	gcg	aac	cac	ggc	tcg	ctg	atc	tcc	ctc	tcg	
1104																
Cys	Trp	Ser	Ile	Ala	Thr	Ala	Asn	His	Gly	Ser	Leu	Ile	Ser	Leu	Ser	
		355					360					365				
agc	ttc	tcg	gcg	atc	ggc	aac	ctg	atg	ggc	aac	ctg	acc	ggc	aac	gtg	
1152																
Ser	Phe	Ser	Ala	Ile	Gly	Asn	Leu	Met	Gly	Asn	Leu	Thr	Gly	Asn	Val	
	370					375					380					
acc	ttg	gaa	ggc	tgg	ctg	gcc	cgc	aag	ttc	tac	att	tcc	ctg	tac	cgc	
1200																
Thr	Leu	Glu	Gly	Trp	Leu	Ala	Arg	Lys	Phe	Tyr	Ile	Ser	Leu	Tyr	Arg	
385					390					395					400	
atg	cac	cag	atg	gcg	ctc	tac	ggc	acc	ttc	cgc	acc	ctg	atg	atg	atg	
1248																
Met	His	Gln	Met	Ala	Leu	Tyr	Gly	Thr	Phe	Arg	Thr	Leu	Met	Met	Met	
				405					410					415		



ctg ggc gac cgc ttc cgc agc agc acc gaa ccc cgc ctc aag ctt cac  
 1296  
 Leu Gly Asp Arg Phe Arg Ser Ser Thr Glu Pro Arg Leu Lys Leu His  
                   420                                  425                                  430

<210> 12  
 <211> 432  
 <212> PRT  
 <213> Azotobacter vinelandii

<400> 12  
 Met Thr His Arg Ile Val Ile Val Gly Gly Gly Ala Gly Gly Val Glu  
   1                                  5                                  10                                  15  
 Leu Ala Thr Arg Leu Gly Lys Thr Met Gly Arg Asn Phe Gln Ala Lys  
                   20                                  25                                  30  
 Ile Thr Leu Val Asp Ala Asn Met Thr His Leu Trp Lys Pro Leu Leu  
                   35                                  40                                  45  
 His Glu Val Ala Ala Gly Ser Leu Asn Ser Thr Gly Asp Glu Leu Asn  
           50                                  55                                  60  
 Tyr Val Ala Gln Ala Lys Trp Asn Asn Phe Glu Phe Gln Tyr Gly Arg  
   65                                  70                                  75                                  80  
 Met Cys Gly Leu Asp Arg Ala Asn Lys Arg Ile Arg Leu Ala Ala Gln  
                   85                                  90                                  95  
 Pro Ala Gln Glu Asp Arg Ala Pro Leu Pro Glu Arg Glu Leu Glu Tyr  
                   100                                  105                                  110  
 Asp Thr Leu Val Leu Ser Val Gly Ser Thr Thr Asn Asp Phe Gly Thr  
           115                                  120                                  125  
 Pro Gly Ala Ala Glu Asn Cys Ile Phe Leu Glu Gly Arg Asp Gln Ala  
   130                                  135                                  140  
 Glu Arg Phe Arg Arg Pro Leu Leu Ser His Tyr Leu Arg Ala His Ala  
   145                                  150                                  155                                  160  
 Ser Asn Asp Asp Gly His Gln Val Lys Val Ala Ile Val Gly Ala Gly  
                   165                                  170                                  175  
 Ala Thr Gly Val Glu Leu Ala Ala Glu Leu Arg His Ala Ser Lys Glu  
                   180                                  185                                  190  
 Leu Val Ala Tyr Gly Leu Glu Arg Ile Pro Pro Glu Asn Leu Ser Ile  
           195                                  200                                  205





<221> CDS  
<222>

<400> 13

ttg	act	aca	cca	tta	aaa	aag	atc	gtg	att	gtc	ggc	ggc	ggc	gct	ggc	48
Met	Thr	Thr	Pro	Leu	Lys	Lys	Ile	Val	Ile	Val	Gly	Gly	Gly	Ala	Gly	
1				5					10					15		
ggg	ctg	gaa	atg	gcg	acg	cag	tta	ggc	cat	aaa	ctg	ggg	cgc	aag	aaa	96
Gly	Leu	Glu	Met	Ala	Thr	Gln	Leu	Gly	His	Lys	Leu	Gly	Arg	Lys	Lys	
			20					25					30			
aaa	gcg	aaa	atc	acg	ctg	gta	gac	aga	aat	cac	agc	cat	ctg	tgg	aaa	144
Lys	Ala	Lys	Ile	Thr	Leu	Val	Asp	Arg	Asn	His	Ser	His	Leu	Trp	Lys	
		35					40					45				
cca	ttg	ctg	cac	gaa	gtg	gcg	act	ggc	tct	ctg	gac	gaa	ggc	gtg	gat	192
Pro	Leu	Leu	His	Glu	Val	Ala	Thr	Gly	Ser	Leu	Asp	Glu	Gly	Val	Asp	
	50					55					60					
gcg	ctg	agc	tat	ctg	gct	cat	gcg	cgt	aat	cat	ggt	ttc	cag	ttc	cag	240
Ala	Leu	Ser	Tyr	Leu	Ala	His	Ala	Arg	Asn	His	Gly	Phe	Gln	Phe	Gln	
65					70					75					80	
ctg	ggg	tcg	gtg	atg	gat	atc	gat	cgc	gaa	gcg	aaa	acc	atc	acc	att	288
Leu	Gly	Ser	Val	Met	Asp	Ile	Asp	Arg	Glu	Ala	Lys	Thr	Ile	Thr	Ile	
				85					90					95		
gcc	gag	ttg	cgt	gat	gaa	aag	ggc	gaa	ctg	ctg	gtg	ccg	gag	cgc	aaa	336
Ala	Glu	Leu	Arg	Asp	Glu	Lys	Gly	Glu	Leu	Leu	Val	Pro	Glu	Arg	Lys	
			100					105					110			
atc	gcg	tat	gac	acg	ctg	gtg	atg	gcg	ctg	ggc	agc	acc	tct	aat	gat	384
Ile	Ala	Tyr	Asp	Thr	Leu	Val	Met	Ala	Leu	Gly	Ser	Thr	Ser	Asn	Asp	
		115					120					125				
ttc	aac	acg	ccg	ggc	gtg	aaa	gag	cac	tgt	atc	ttc	ctc	gat	aac	ccg	432
Phe	Asn	Thr	Pro	Gly	Val	Lys	Glu	His	Cys	Ile	Phe	Leu	Asp	Asn	Pro	
	130					135					140					
cat	cag	gcg	cgc	cgt	ttt	cac	cag	gag	atg	ctg	aac	ctg	ttc	ctc	aag	480
His	Gln	Ala	Arg	Arg	Phe	His	Gln	Glu	Met	Leu	Asn	Leu	Phe	Leu	Lys	
145					150					155					160	
tat	tcg	gct	aat	ctg	ggc	gcg	aac	ggt	aag	gtc	aat	atc	gcc	atc	gtt	528
Tyr	Ser	Ala	Asn	Leu	Gly	Ala	Asn	Gly	Lys	Val	Asn	Ile	Ala	Ile	Val	
				165					170					175		

ggc Gly	ggc Gly	ggt Gly	gcg Ala 180	acg Thr	ggg Gly	gtt Val	gag Glu	ctg Leu 185	tcg Ser	gct Ala	gaa Glu	ctg Leu	cat His 190	aat Asn	gcg Ala	576
gta Val	aaa Lys	cag Gln 195	ctg Leu	cat His	agc Ser	tat Tyr	ggt Gly 200	tat Tyr	aag Lys	ggg Gly	ctg Leu	acc Thr 205	aac Asn	gac Asp	gcg Ala	624
ctg Leu	aac Asn 210	gtg Val	acg Thr	ttg Leu	gtt Val	gag Glu 215	gct Ala	ggc Gly	gag Glu	cgt Arg	att Ile 220	ctg Leu	cct Pro	gcg Ala	ttg Leu	672
ccg Pro 225	ccg Pro	cgt Arg	atc Ile	tcc Ser	agc Ser 230	gcc Ala	gcg Ala	cat His	aat Asn	gaa Glu 235	ctg Leu	acc Thr	aaa Lys	ctg Leu	ggc Gly 240	720
gtt Val	cgc Arg	gtg Val	ctg Leu	acg Thr 245	caa Gln	act Thr	atg Met	gtc Val	acc Thr 250	agc Ser	gcc Ala	gac Asp	gaa Glu	ggc Gly 255	ggt Gly	768
ctg Leu	cat His	acg Thr	aaa Lys 260	gaa Glu	ggt Gly	gaa Glu	tat Tyr	att Ile 265	cag Gln	gcc Ala	gat Asp	ctg Leu	atg Met 270	gtg Val	tgg Trp	816
gcg Ala	gcg Ala	ggt Gly 275	atc Ile	aaa Lys	gcg Ala	cca Pro	gat Asp 280	ttt Phe	atg Met	aaa Lys	gag Glu	att Ile 285	ggt Gly	ggt Gly	ctg Leu	864
gaa Glu	acg Thr 290	aac Asn	cgc Arg	att Ile	aac Asn	caa Gln 295	ctg Leu	gtg Val	gtg Val	gaa Glu	ccg Pro 300	acg Thr	ctg Leu	caa Gln	acc Thr	912
acg Thr 305	cgc Arg	gat Asp	cct Pro	gat Asp	att Ile 310	tat Tyr	gcg Ala	att Ile	ggc Gly	gac Asp 315	tgc Cys	gct Ala	tcc Ser	tgc Cys	gca Ala 320	960
cgt 1008 Arg	ccg Pro	gag Glu	gga Gly	ggt Gly 325	ttt Phe	gtg Val	ccg Pro	cct Pro	cgc Arg 330	gct Ala	cag Gln	gcg Ala	gcg Ala	cat His 335	cag Gln	
atg 1056 Met	gct Ala	acc Thr	tgc Cys 340	gcg Ala	atg Met	aaa Lys	aac Asn	att Ile 345	ctg Leu	gcg Ala	cag Gln	atg Met	aat Asn 350	ggc Gly	aaa Lys	
ccg 1104 Pro	ctg Leu	aaa Lys 355	gct Ala	tac Tyr	cag Gln	tat Tyr	aaa Lys 360	gat Asp	cat His	gga Gly	tcg Ser	ctg Leu 365	gtc Val	tct Ser	ctg Leu	

tcc aac ttc tct acc gtg ggt agt ctg atg ggg aac ctg acc cgc ggt  
 1152  
 Ser Asn Phe Ser Thr Val Gly Ser Leu Met Gly Asn Leu Thr Arg Gly  
 370 375 380

tca atg atg att gaa gga cgt atc gcc cgc ttc gtg tat atc tcg cta  
 1200  
 Ser Met Met Ile Glu Gly Arg Ile Ala Arg Phe Val Tyr Ile Ser Leu  
 385 390 395 400

tac cgt atg cac cag ata gcg ctg cat gga tac ttt aaa acc ggc ctg  
 1248  
 Tyr Arg Met His Gln Ile Ala Leu His Gly Tyr Phe Lys Thr Gly Leu  
 405 410 415

atg atg ctg gtg ggc agt att aac cgc gtc att cgt ccg cgc ctg aaa  
 1296  
 Met Met Leu Val Gly Ser Ile Asn Arg Val Ile Arg Pro Arg Leu Lys  
 420 425 430

ctg cat 1302  
 Leu His

<210> 14  
 <211> 434  
 <212> PRT  
 <213> Salmonella typhimurium LT2

<400> 14  
 Met Thr Thr Pro Leu Lys Lys Ile Val Ile Val Gly Gly Gly Ala Gly  
 1 5 10 15  
 Gly Leu Glu Met Ala Thr Gln Leu Gly His Lys Leu Gly Arg Lys Lys  
 20 25 30  
 Lys Ala Lys Ile Thr Leu Val Asp Arg Asn His Ser His Leu Trp Lys  
 35 40 45  
 Pro Leu Leu His Glu Val Ala Thr Gly Ser Leu Asp Glu Gly Val Asp  
 50 55 60  
 Ala Leu Ser Tyr Leu Ala His Ala Arg Asn His Gly Phe Gln Phe Gln  
 65 70 75 80  
 Leu Gly Ser Val Met Asp Ile Asp Arg Glu Ala Lys Thr Ile Thr Ile  
 85 90 95  
 Ala Glu Leu Arg Asp Glu Lys Gly Glu Leu Leu Val Pro Glu Arg Lys  
 100 105 110

Ile	Ala	Tyr	Asp	Thr	Leu	Val	Met	Ala	Leu	Gly	Ser	Thr	Ser	Asn	Asp
		115					120					125			
Phe	Asn	Thr	Pro	Gly	Val	Lys	Glu	His	Cys	Ile	Phe	Leu	Asp	Asn	Pro
	130					135					140				
His	Gln	Ala	Arg	Arg	Phe	His	Gln	Glu	Met	Leu	Asn	Leu	Phe	Leu	Lys
145					150					155					160
Tyr	Ser	Ala	Asn	Leu	Gly	Ala	Asn	Gly	Lys	Val	Asn	Ile	Ala	Ile	Val
				165					170					175	
Gly	Gly	Gly	Ala	Thr	Gly	Val	Glu	Leu	Ser	Ala	Glu	Leu	His	Asn	Ala
			180					185					190		
Val	Lys	Gln	Leu	His	Ser	Tyr	Gly	Tyr	Lys	Gly	Leu	Thr	Asn	Asp	Ala
		195					200					205			
Leu	Asn	Val	Thr	Leu	Val	Glu	Ala	Gly	Glu	Arg	Ile	Leu	Pro	Ala	Leu
	210					215					220				
Pro	Pro	Arg	Ile	Ser	Ser	Ala	Ala	His	Asn	Glu	Leu	Thr	Lys	Leu	Gly
225					230					235					240
Val	Arg	Val	Leu	Thr	Gln	Thr	Met	Val	Thr	Ser	Ala	Asp	Glu	Gly	Gly
				245					250					255	
Leu	His	Thr	Lys	Glu	Gly	Glu	Tyr	Ile	Gln	Ala	Asp	Leu	Met	Val	Trp
			260					265					270		
Ala	Ala	Gly	Ile	Lys	Ala	Pro	Asp	Phe	Met	Lys	Glu	Ile	Gly	Gly	Leu
		275					280					285			
Glu	Thr	Asn	Arg	Ile	Asn	Gln	Leu	Val	Val	Glu	Pro	Thr	Leu	Gln	Thr
	290					295					300				
Thr	Arg	Asp	Pro	Asp	Ile	Tyr	Ala	Ile	Gly	Asp	Cys	Ala	Ser	Cys	Ala
305					310					315					320
Arg	Pro	Glu	Gly	Gly	Phe	Val	Pro	Pro	Arg	Ala	Gln	Ala	Ala	His	Gln
				325					330					335	
Met	Ala	Thr	Cys	Ala	Met	Lys	Asn	Ile	Leu	Ala	Gln	Met	Asn	Gly	Lys
			340					345					350		
Pro	Leu	Lys	Ala	Tyr	Gln	Tyr	Lys	Asp	His	Gly	Ser	Leu	Val	Ser	Leu
		355					360					365			
Ser	Asn	Phe	Ser	Thr	Val	Gly	Ser	Leu	Met	Gly	Asn	Leu	Thr	Arg	Gly

370		375		380
Ser 385	Met Met Ile Glu Gly 390	Arg Ile Ala Arg Phe 395	Val Tyr Ile Ser Leu 400	
Tyr	Arg Met His Gln 405	Ile Ala Leu His Gly 410	Tyr Phe Lys Thr Gly 415	Leu
Met Met Leu 420	Val Gly Ser Ile Asn Arg 425	Val Ile Arg Pro Arg 430	Leu Lys	

Leu His

<210> 15

<211> 1908

<212> DNA

<213> Lactobacillus plantarum WCFS1

<220>

<221> CDS

<222>

<400> 15

atg gca aag aaa aat att gtc gtt gtc ggt gcg ggg ttt gct ggt gtt	48
Met Ala Lys Lys Asn Ile Val Val Val Gly Ala Gly Phe Ala Gly Val	
1 5 10 15	
tac gca acc aag aaa ctg tct aag cat ttc aaa aaa aat gca gac gtc	96
Tyr Ala Thr Lys Lys Leu Ser Lys His Phe Lys Lys Asn Ala Asp Val	
20 25 30	
gag att acg ttg att gac cgg cat tca tac ttc acg tat atg act gaa	144
Glu Ile Thr Leu Ile Asp Arg His Ser Tyr Phe Thr Tyr Met Thr Glu	
35 40 45	
tta cat gaa gtt gct acc gaa cgg gtg gaa cct gag cat atc caa tat	192
Leu His Glu Val Ala Thr Glu Arg Val Glu Pro Glu His Ile Gln Tyr	
50 55 60	
gat ttg caa cgg ttg ttc gca cgg cga aaa aac gtt cgt ctc gtg acc	240
Asp Leu Gln Arg Leu Phe Ala Arg Arg Lys Asn Val Arg Leu Val Thr	
65 70 75 80	
gat acc gtg acg ggc atc gac aaa aag gca caa aca gtt act acc gaa	288
Asp Thr Val Thr Gly Ile Asp Lys Lys Ala Gln Thr Val Thr Thr Glu	
85 90 95	
cac gga agt tat caa tat gat caa ctt tta att agt ttg ggt ggg gaa	336



His	Gly	Ser	Tyr	Gln	Tyr	Asp	Gln	Leu	Leu	Ile	Ser	Leu	Gly	Gly	Glu	
			100					105					110			
tcc	aat	gac	ttt	ggg	act	ccc	ggt	gtt	aag	gaa	cac	ggc	ttc	gaa	ttg	384
Ser	Asn	Asp	Phe	Gly	Thr	Pro	Gly	Val	Lys	Glu	His	Gly	Phe	Glu	Leu	
		115					120					125				
tgg	tcc	ttc	gaa	caa	gcg	atg	gca	ttg	cgc	gct	cac	tta	tct	gca	att	432
Trp	Ser	Phe	Glu	Gln	Ala	Met	Ala	Leu	Arg	Ala	His	Leu	Ser	Ala	Ile	
	130					135					140					
att	cgg	cgg	ggg	gcg	gcg	gag	ctc	gac	cct	gct	aag	cgc	aaa	gcc	atg	480
Ile	Arg	Arg	Gly	Ala	Ala	Glu	Leu	Asp	Pro	Ala	Lys	Arg	Lys	Ala	Met	
145					150					155					160	
ttg	acc	ttt	aca	gtc	tgt	ggt	tct	ggt	ttt	act	ggt	tct	gaa	ctg	att	528
Leu	Thr	Phe	Thr	Val	Cys	Gly	Ser	Gly	Phe	Thr	Gly	Ser	Glu	Leu	Ile	
				165					170					175		
ggt	gaa	tta	atc	gaa	tat	cgt	gat	gtt	ttg	gct	cga	gac	aac	aag	ctc	576
Gly	Glu	Leu	Ile	Glu	Tyr	Arg	Asp	Val	Leu	Ala	Arg	Asp	Asn	Lys	Leu	
			180					185					190			
gat	cca	agt	gaa	atc	acg	ctc	caa	ttg	gtc	gaa	gca	gcg	ccg	act	att	624
Asp	Pro	Ser	Glu	Ile	Thr	Leu	Gln	Leu	Val	Glu	Ala	Ala	Pro	Thr	Ile	
		195					200					205				
att	aac	atg	ctc	aac	cgg	acg	caa	gcc	ggt	aag	gcc	gct	aag	tac	atg	672
Ile	Asn	Met	Leu	Asn	Arg	Thr	Gln	Ala	Gly	Lys	Ala	Ala	Lys	Tyr	Met	
	210					215					220					
gaa	aaa	cat	ggt	gtc	aaa	atc	atg	acg	aac	tcc	atg	att	acc	gaa	gtc	720
Glu	Lys	His	Gly	Val	Lys	Ile	Met	Thr	Asn	Ser	Met	Ile	Thr	Glu	Val	
225					230					235					240	
tgt	gaa	gac	cat	gtt	aac	tta	aaa	ggc	aag	gat	cca	att	cca	acc	tac	768
Cys	Glu	Asp	His	Val	Asn	Leu	Lys	Gly	Lys	Asp	Pro	Ile	Pro	Thr	Tyr	
				245					250					255		
acg	tta	atc	tgg	aca	gcc	ggt	gtt	cgt	gct	aat	agt	atc	gtt	aaa	aag	816
Thr	Leu	Ile	Trp	Thr	Ala	Gly	Val	Arg	Ala	Asn	Ser	Ile	Val	Lys	Lys	
			260					265					270			
ttc	ggc	att	gaa	act	aac	ccc	cgc	ggt	ggt	cgc	ttg	atg	gcc	aat	gaa	864
Phe	Gly	Ile	Glu	Thr	Asn	Pro	Arg	Gly	Gly	Arg	Leu	Met	Ala	Asn	Glu	
		275					280					285				
ttc	atg	caa	gct	aag	gat	tgt	aac	aat	atc	ttc	tta	gcc	ggt	gat	tca	912
Phe	Met	Gln	Ala	Lys	Asp	Cys	Asn	Asn	Ile	Phe	Leu	Ala	Gly	Asp	Ser	
	290					295					300					



acc agc tac caa gaa cct gac caa cca cgg cca gtc cca caa atc gtt 960  
 Thr Ser Tyr Gln Glu Pro Asp Gln Pro Arg Pro Val Pro Gln Ile Val  
 305 310 315 320

caa ggg gct gaa gaa acc gca gct aag gcc gtc gaa ggt att att aag  
 1008  
 Gln Gly Ala Glu Glu Thr Ala Ala Lys Ala Val Glu Gly Ile Ile Lys  
 325 330 335

aac gtt gac cag act gac gtt acg atc aag cca ttt aag ggc gct tat  
 1056  
 Asn Val Asp Gln Thr Asp Val Thr Ile Lys Pro Phe Lys Gly Ala Tyr  
 340 345 350

caa gca tcc gtc gac tca att ggt tcc aaa tat gcc gtt gca caa gtt  
 1104  
 Gln Ala Ser Val Asp Ser Ile Gly Ser Lys Tyr Ala Val Ala Gln Val  
 355 360 365

tta gag aag tgg aac gtc tct ggt ttt att gcc gtg ctt tta aaa cac  
 1152  
 Leu Glu Lys Trp Asn Val Ser Gly Phe Ile Ala Val Leu Leu Lys His  
 370 375 380

gcc atc aac tgg atg tac tac gtt cag att ttc tca ggt tac tac cta  
 1200  
 Ala Ile Asn Trp Met Tyr Tyr Val Gln Ile Phe Ser Gly Tyr Tyr Leu  
 385 390 395 400

ttc cag tac ttc atg cac gaa ttc ttc cgg act cgt aat aac cgt aac  
 1248  
 Phe Gln Tyr Phe Met His Glu Phe Phe Arg Thr Arg Asn Asn Arg Asn  
 405 410 415

gtc ttc cgc ggt tgg gtc tca cgg gct ggt aac gta ctc tgg agt gtg  
 1296  
 Val Phe Arg Gly Trp Val Ser Arg Ala Gly Asn Val Leu Trp Ser Val  
 420 425 430

cca ctg cgg ttc ttc tat ggt gcc atg tgg tta tgg gac tgc tgg act  
 1344  
 Pro Leu Arg Phe Phe Tyr Gly Ala Met Trp Leu Trp Asp Cys Trp Thr  
 435 440 445

aaa gtt cag gga tct gaa tcc tgg ttc act gac aag tta cgg tta cca  
 1392  
 Lys Val Gln Gly Ser Glu Ser Trp Phe Thr Asp Lys Leu Arg Leu Pro  
 450 455 460

ttc gaa tgg att acc gtg gcc gca acc agt ggt gcc tct caa gca act  
 1440  
 Phe Glu Trp Ile Thr Val Ala Ala Thr Ser Gly Ala Ser Gln Ala Thr  
 465 470 475 480

aaa gcc gct gca acc agt ggt gct tct gaa gct gcc acg tca acc gtt  
 1488  
 Lys Ala Ala Ala Thr Ser Gly Ala Ser Glu Ala Ala Thr Ser Thr Val  
 485 490 495

aaa gcc gct aag ggt gtc ttc agt ctt tca tac atg tac ggt aaa gaa  
 1536  
 Lys Ala Ala Lys Gly Val Phe Ser Leu Ser Tyr Met Tyr Gly Lys Glu  
 500 505 510

ccc ctg atg gtc ttt gac aaa atg cca cat tgg ttc gaa tca att acc  
 1584  
 Pro Leu Met Val Phe Asp Lys Met Pro His Trp Phe Glu Ser Ile Thr  
 515 520 525

aag gtc ttc att ccg aac atg caa atg gcc ctc ttc ttc cag aaa ttc  
 1632  
 Lys Val Phe Ile Pro Asn Met Gln Met Ala Leu Phe Phe Gln Lys Phe  
 530 535 540

atg act tgt gtt gaa atc gtc att gca tta tgt att ttc ttc gga ctc  
 1680  
 Met Thr Cys Val Glu Ile Val Ile Ala Leu Cys Ile Phe Phe Gly Leu  
 545 550 555 560

ttt act tgg ttt gct aac gca gtc acc att ggc tta gtt gtc gtc ttc  
 1728  
 Phe Thr Trp Phe Ala Asn Ala Val Thr Ile Gly Leu Val Val Val Phe  
 565 570 575

tgc tta tct ggc atg ttc tac tgg gtc aac att tgg atg atc ttt gtt  
 1776  
 Cys Leu Ser Gly Met Phe Tyr Trp Val Asn Ile Trp Met Ile Phe Val  
 580 585 590

gcc ctc gcc tta atg aac ggt tcc gga cgg aca ttt ggg tta gac tac  
 1824  
 Ala Leu Ala Leu Met Asn Gly Ser Gly Arg Thr Phe Gly Leu Asp Tyr  
 595 600 605

tgg gtc gtt ccg tgg atg caa aaa cac ctt gga cac tgg tgg tac ggc  
 1872  
 Trp Val Val Pro Trp Met Gln Lys His Leu Gly His Trp Trp Tyr Gly  
 610 615 620

aac gtt cgt tct cat tac gac ggt gtt aaa acc cgc  
 Asn Val Arg Ser His Tyr Asp Gly Val Lys Thr Arg  
 625 630 635

1908

<210> 16  
 <211> 636  
 <212> PRT  
 <213> Lactobacillus plantarum WCFS1

<400> 16  
 Met Ala Lys Lys Asn Ile Val Val Val Gly Ala Gly Phe Ala Gly Val  
 1 5 10 15  
 Tyr Ala Thr Lys Lys Leu Ser Lys His Phe Lys Lys Asn Ala Asp Val  
 20 25 30  
 Glu Ile Thr Leu Ile Asp Arg His Ser Tyr Phe Thr Tyr Met Thr Glu  
 35 40 45  
 Leu His Glu Val Ala Thr Glu Arg Val Glu Pro Glu His Ile Gln Tyr  
 50 55 60  
 Asp Leu Gln Arg Leu Phe Ala Arg Arg Lys Asn Val Arg Leu Val Thr  
 65 70 75 80  
 Asp Thr Val Thr Gly Ile Asp Lys Lys Ala Gln Thr Val Thr Thr Glu  
 85 90 95  
 His Gly Ser Tyr Gln Tyr Asp Gln Leu Leu Ile Ser Leu Gly Gly Glu  
 100 105 110  
 Ser Asn Asp Phe Gly Thr Pro Gly Val Lys Glu His Gly Phe Glu Leu  
 115 120 125  
 Trp Ser Phe Glu Gln Ala Met Ala Leu Arg Ala His Leu Ser Ala Ile  
 130 135 140  
 Ile Arg Arg Gly Ala Ala Glu Leu Asp Pro Ala Lys Arg Lys Ala Met  
 145 150 155 160  
 Leu Thr Phe Thr Val Cys Gly Ser Gly Phe Thr Gly Ser Glu Leu Ile  
 165 170 175  
 Gly Glu Leu Ile Glu Tyr Arg Asp Val Leu Ala Arg Asp Asn Lys Leu  
 180 185 190  
 Asp Pro Ser Glu Ile Thr Leu Gln Leu Val Glu Ala Ala Pro Thr Ile  
 195 200 205  
 Ile Asn Met Leu Asn Arg Thr Gln Ala Gly Lys Ala Ala Lys Tyr Met

210					215					220					
Glu 225	Lys	His	Gly	Val	Lys 230	Ile	Met	Thr	Asn	Ser 235	Met	Ile	Thr	Glu	Val 240
Cys	Glu	Asp	His	Val 245	Asn	Leu	Lys	Gly	Lys 250	Asp	Pro	Ile	Pro	Thr 255	Tyr
Thr	Leu	Ile	Trp 260	Thr	Ala	Gly	Val	Arg 265	Ala	Asn	Ser	Ile	Val 270	Lys	Lys
Phe	Gly	Ile 275	Glu	Thr	Asn	Pro	Arg 280	Gly	Gly	Arg	Leu	Met 285	Ala	Asn	Glu
Phe 290	Met	Gln	Ala	Lys	Asp	Cys 295	Asn	Asn	Ile	Phe	Leu 300	Ala	Gly	Asp	Ser
Thr 305	Ser	Tyr	Gln	Glu	Pro 310	Asp	Gln	Pro	Arg	Pro 315	Val	Pro	Gln	Ile	Val 320
Gln	Gly	Ala	Glu	Glu 325	Thr	Ala	Ala	Lys	Ala 330	Val	Glu	Gly	Ile	Ile 335	Lys
Asn	Val	Asp	Gln 340	Thr	Asp	Val	Thr	Ile 345	Lys	Pro	Phe	Lys	Gly 350	Ala	Tyr
Gln	Ala	Ser 355	Val	Asp	Ser	Ile	Gly 360	Ser	Lys	Tyr	Ala	Val 365	Ala	Gln	Val
Leu 370	Glu	Lys	Trp	Asn	Val	Ser 375	Gly	Phe	Ile	Ala	Val 380	Leu	Leu	Lys	His
Ala 385	Ile	Asn	Trp	Met	Tyr 390	Tyr	Val	Gln	Ile	Phe 395	Ser	Gly	Tyr	Tyr	Leu 400
Phe	Gln	Tyr	Phe	Met 405	His	Glu	Phe	Phe	Arg 410	Thr	Arg	Asn	Asn	Arg 415	Asn
Val	Phe	Arg	Gly 420	Trp	Val	Ser	Arg	Ala 425	Gly	Asn	Val	Leu	Trp 430	Ser	Val
Pro	Leu	Arg 435	Phe	Phe	Tyr	Gly	Ala 440	Met	Trp	Leu	Trp	Asp 445	Cys	Trp	Thr
Lys 450	Val	Gln	Gly	Ser	Glu	Ser 455	Trp	Phe	Thr	Asp	Lys 460	Leu	Arg	Leu	Pro
Phe 465	Glu	Trp	Ile	Thr	Val 470	Ala	Ala	Thr	Ser	Gly 475	Ala	Ser	Gln	Ala	Thr 480

Lys Ala Ala Ala Thr Ser Gly Ala Ser Glu Ala Ala Thr Ser Thr Val  
485 490 495

Lys Ala Ala Lys Gly Val Phe Ser Leu Ser Tyr Met Tyr Gly Lys Glu  
500 505 510

Pro Leu Met Val Phe Asp Lys Met Pro His Trp Phe Glu Ser Ile Thr  
515 520 525

Lys Val Phe Ile Pro Asn Met Gln Met Ala Leu Phe Phe Gln Lys Phe  
530 535 540

Met Thr Cys Val Glu Ile Val Ile Ala Leu Cys Ile Phe Phe Gly Leu  
545 550 555 560

Phe Thr Trp Phe Ala Asn Ala Val Thr Ile Gly Leu Val Val Val Phe  
565 570 575

Cys Leu Ser Gly Met Phe Tyr Trp Val Asn Ile Trp Met Ile Phe Val  
580 585 590

Ala Leu Ala Leu Met Asn Gly Ser Gly Arg Thr Phe Gly Leu Asp Tyr  
595 600 605

Trp Val Val Pro Trp Met Gln Lys His Leu Gly His Trp Trp Tyr Gly  
610 615 620

Asn Val Arg Ser His Tyr Asp Gly Val Lys Thr Arg  
625 630 635